A NOVEL APPROACH TO PHOSPHOPEPTIDE SYNTHESIS-PREPARATION OF GLU-PSER-LEU P.F. Alewood^{*}, J.W. Perich and R.B. Johns Department of Organic Chemistry, University of Melbourne, Parkville, Victoria 3052, Australia.

<u>ABSTRACT</u>: A synthesis of the phosphotripeptide Glu-PSer-Leu is reported via the stepwise incorporation of the protected phosphoamino acid N^α-tert-butoxycarbonyl-Odibenzylphosphono-L-serine.

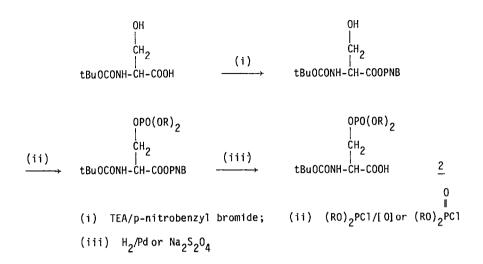
Our interest in the structure and reactivity of the heavily phosphorylated area of the α and β caseins has lead to the choice of the homologous region (<u>1</u>) and its congeners as synthetic targets.

We wish to describe in this letter our strategy and methodology for constructing complex phosphorylated sequences through the preparation of the tripeptide, Glu-PSer-Leu (5).

Our initial attempts¹ to generate phosphopeptides using traditional procedures² were frustrated by complex mixtures. In our hands, the use of phosphochloridates, $(RO)_2POC1$ as phosphorylating agents for peptide substrates gave either incomplete phosphorylation (for R=Bz1) or partial deprotection on hydrogenation (for R=C₆H₅). A more serious limitation to this 'Total Phosphorylation' approach is its incompatibility with the preparation of specifically phosphorylated peptides e.g., -Ser-PSer-Glu-Glu-.

To avoid the difficulties inherent in former approaches we chose the novel strategy which incorporates the phosphate group as a suitably protected phosphoamino acid (2).

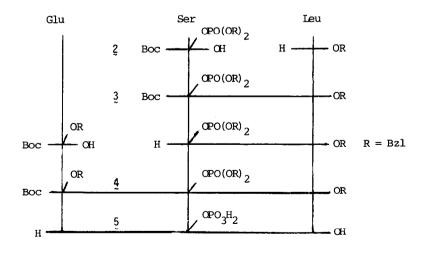
The synthesis of 2 is outlined in Scheme 1 and experimental details are provided elsewhere^{3,4}.



Scheme 1

We now wish to report the inclusion of $\underline{2}$ (R=Bz1) in the synthetic sequence Glu-PSer-Leu ($\underline{5}$) via solution phase methodology. The phosphopeptide segment $\underline{5}$ occurs both in casein and in bovine enamel peptide sequences. These have been postulated to be important Ca²⁺ binding sites, playing roles in micelle stabilization⁵ and enamel calcification.

The synthesis of 5 is outlined below (Scheme 2).



All couplings were performed using the excess mixed anhydride procedure^{7,8}. Coupling yields were 95% and 80% respectively for the intermediate protected peptides 3^{11} and 4^{12} which were homogeneous by tlc criteria. These species were readily characterised by their ¹H, ¹³C and ³¹P nmr spectra^{13,14}. ³¹P nmr values¹⁵ of -0.9 and -0.8 ppm, typical of phosphotriesters, were observed for peptides 3 and 4, respectively.

'Debocking' of the intermediate peptide <u>3</u> was achieved using 98% formic acid. This was necessary as the usual acidolytic reagents (4M HCl/dioxan, CF_3COOH/CH_2Cl_2) caused considerable debenzylation of the phosphotriester functionality, as observed by ³¹P nmr. We will report on the stability of protected phosphoserine residues incorporated in a peptide chain at a later date.

A one step deprotection of $\underline{4}$ was achieved quantitatively by hydrogenolysis using 10% Pd/C in formic acid. This gave pure $\underline{5}$ as white flakes, $[\alpha]_D^{21}$ - 14.0 (C4, 1M HC1). The HPLC profile (μ Bondapak C18, 0-50% CH₂CN/.1% TEAP pH 4.0, 1m1/min, 214 nm) showed a single peak and ¹H, ¹³C and ³¹P nmr spectra¹⁶ were assigned and contained no additional contaminant resonances. A satisfactory amino acid analysis was obtained¹⁷.

By several criteria this synthesis has increased our confidence in the incorporation of protected phosphoserine residues into a growing peptide chain. The high coupling yields achieved and the stability of the resultant phosphotriester together with a simple final deprotection step suggest future phosphopeptide syntheses along these lines to be a viable proposition.

<u>ACKNOWLEDGEMENT</u>: The authors gratefully acknowledge support from the Australian Dairy Corporation.

NOTES AND REFERENCES

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- 8. The optical integrity of the phosphoamino acid coupling step was confirmed by the conversion of 3 (H₂, Pd/C, HCOOH) to the known phosphodipeptide PSer-Leu; $[\alpha]_D^{21}$ -15.0 (C4, 1M HC1) lit.⁹ $[\alpha]_D^{21}$ -16.0 (C4, 1M HC1); lit.¹⁰ [(d)PSer-Leu], $[\alpha]_D^{21}$ -28.1 (C3.6, 1M HC1).
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- 11. In the coupling of synthon $\underline{2}$ to Leu-OBzl, ether was the workup solvent of choice to avoid contamination of the dipeptide 3 with excess sodium salt of $\underline{2}$.
- 12. 4 required flash chromatography on silica gel due to baseline impurities.
- 13. ¹³C nmr δ(CDCl₃) <u>3</u>: 171.8, 168.4, 155.0, 135.2 (d, J=5.86Hz) 135.0, 128.2, 127.9, 127.7, 80.0, 69.2 (d, J=5.86Hz), 66.5, 66.5 (unresolved doublet), 54.1 (d, J=5.86Hz), 50.7, 40.8, 27.9, 24.3, 22.4, 21.5, 18.7.
- 14. ¹³C nmr δ(CDCl₃) 4; 173.0, 171.9, 168.1, 155.7, 135.4, 135.3 (d, J=5.86Hz), 135.5, 128.6, 128.2, 128.1, 80.3, 69.6 (d, J=5.86Hz), 66.8, 66.8 (unresolved doublet), 66.7, 54.3, 53.2 (d, J=5.86Hz), 51.2, 40.8, 30.4, 28.3, 27.4, 24.7, 22.8, 21.8.
- 15. Relative to 85% H₂PO₄.
- 16. ¹³C nmr $\delta(H_20)$ <u>5</u>; 176.6, 176.6, 170.6, 169.7, 64.5 (d, J=5.86Hz), 54.6 (d, J=5.86Hz), 52.7, 52.1, 39.9, 29.6, 26.3, 24.9, 22.7, 21.1. ³¹P nmr $\delta(H_20)$ <u>5</u>; 1 peak, + 0.3.
- 17. Amino acid analysis (6M HCl, 105°): Glu 0.97 (1); Ser 0.88 (1); Leu 1.00 (1); Ala 0.01. The presence of Ala arises from β elimination and subsequent hydrogenation of the resulting dehydrotripeptide.

(Received in UK 14 December 1983)